

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: February 16, 2005, 16:16:11 ; Search time 15.6881 Seconds
(without alignments)
2330.584 Million cell updates/sec
Title: US-10-003-356-5
Perfect score: 1986
Sequence: 1 LPHSVCTDVCPPGTGCGFVQ.....TVSTVLDDRLVLYMCPLKIQ 380
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	%			DB	ID	Description
	Score	Match	Length			
1	714.5	36.0	1079	2	I59362	calcium/polyvalent
2	711.5	35.8	1078	2	A56715	calcium receptor (
3	711.5	35.8	1088	2	B56715	calcium receptor (
4	709.5	35.7	1085	2	S40476	Ca(2+)-sensing rec
5	431.5	21.7	858	2	JC7683	taste receptor T1R
6	415.5	20.9	879	2	JH0562	metabotropic gluta
7	415.5	20.9	879	2	JH0562	metabotropic gluta
8	409.5	20.6	872	2	JH0561	metabotropic gluta
9	397.5	20.0	1180	2	JC2132	metabotropic gluta
10	397.5	20.0	1199	2	A41939	G protein-coupled
11	397.5	20.0	1212	2	JC2131	metabotropic gluta
12	396.5	20.0	1171	2	A42916	metabotropic gluta
13	383	19.3	1218	2	S71376	glutamate receptor
14	353	17.8	999	2	T27628	hypothetical prote
15	324	16.3	915	2	A49874	metabotropic gluta
16	323	16.3	1267	2	T21340	hypothetical prote
17	309	15.6	871	2	A46742	metabotropic gluta
18	308	15.5	912	2	JH0563	metabotropic gluta
19	295	14.9	908	2	I49142	metabotropic gluta
20	284.5	14.3	551	2	T30806	metabotropic gluta
21	207.5	10.4	1099	2	T16283	hypothetical prote
22	125	6.3	354	2	T33395	hypothetical prote
23	119	6.0	377	2	A69277	Na+/H+ antiporter
24	117	5.9	893	2	A47550	bride of sevenless
25	115.5	5.8	486	2	S51503	NADH2 dehydrogenas
26	112	5.6	896	2	S26740	gene boss protein
27	112	5.6	896	2	A36455	bride of sevenless
28	110.5	5.6	410	2	E84998	hypothetical prote
29	109	5.5	332	2	T21399	hypothetical prote

30 108.5 5.5 403 2 G71236 hypothetical prote
31 108 5.4 464 2 B64173 hypothetical prote
32 105 5.3 887 2 S73768 MG277 homolog F11
33 104.5 5.3 1400 2 A81672 secDF protein, pro
34 104 5.2 437 2 A88942 protein R13D11.3
35 103.5 5.2 469 2 D84949 NADH2 dehydrogenas
36 103 5.2 411 2 AF0203 probable membrane
37 103 5.2 552 2 T25496 hypothetical prote
38 102 5.2 592 2 E82939 transport ATP-bind
39 102 5.1 405 2 F89930 hypothetical prote
40 102 5.1 540 2 T43747 NADH2 dehydrogenas
41 100.5 5.1 610 2 S19461 probable membrane
42 100.5 5.1 825 2 T46311 hypothetical prote
43 100 5.0 437 2 H47070 probable O-antigen
44 100 5.0 461 2 H64636 proline/betaine tr
45 99.5 5.0 344 2 T30984 hypothetical prote

ALIGNMENTS

RESULT 1

I59362
calcium/polyvalent cation-sensing receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I59362; A55594
R:Ruut, M.; Molliver, M.E.; Snowden, A.M.; Snyder, S.H.
Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995
A:Title: Calcium sensing receptor: molecular cloning in rat and localization to nerve t.
A:Reference number: I59362; MUID:95241465; PMID:7724534
A:Accession: I59362
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1079 <RES>
A:Cross-references: UNIPROT:P48442; EMBL:U20289; NID:g790578; PIDN:AAC52195.1; PID:g790
A:Experimental source: striatal
R:Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C.
Proc. Natl. Acad. Sci. U.S.A. 92, 131-135, 1995
A:Title: Cloning and functional expression of a rat kidney extracellular calcium/polyva
A:Reference number: A55594; MUID:95116508; PMID:7816802
A:Accession: A55594
A:Molecule type: mRNA
A:Residues: 1-133,'X',135-1079 <RIC>
A:Cross-references: GB:U10354
A:Experimental source: kidney
C:Keywords: calcium; glycoprotein; phosphoprotein; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:187-212/Region: hydrophobic
F:613-635/Domain: transmembrane #status predicted <TM1>
F:650-670/Domain: transmembrane #status predicted <TM2>
F:683-700/Domain: transmembrane #status predicted <TM3>
F:725-744/Domain: transmembrane #status predicted <TM4>
F:770-790/Domain: transmembrane #status predicted <TM5>
F:806-828/Domain: transmembrane #status predicted <TM6>
F:841-860/Domain: transmembrane #status predicted <TM7>
F:90,261,287,386,488,594,893,1005/Binding site: carbohydrate (Asn) (covalent) #statu
F:794/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicte
F:899,903/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predic

Query Match 36.0%; Score 714.5; DB 2; Length 1079;
Best Local Similarity 38.3%; Pred. No. 4.7e-50;
Matches 146; Conservative 71; Mismatches 137; Indels 27; Gaps 6;

QY 1 LPHSVCTDVCPPGTGCGFVQREPICCFDSIPCADGHVSKPGERCEQCQGEYWSNAQKS 60
DB 537 VPFVNSCRDCQAGTRKRIIEGPTCCFCEVCPEGYSGETDASACDKCPDDFWNSNHT 596
QY 61 ECVLKEVEYLAYDEALGFTLVLSVFGAFVLAATAVAVVIHRTPLVNASDWQLGFLIQV 120
DB 597 SCIAKIEFLAWTEFPFGALTFLFVLGIFLTFVGLGVFKFNTPLVKATNELSVLLFP 656
QY 121 SLIIMLLSSMLPIDKPHNWSMAGQVTLALGFSCLSLGKTSLSFLAYRISKSTQLT 180

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Db      657 SLLCCFSSLPFGEPQDWTCLRPAPFGISFVLCISCLVKTNRVLLVF---EAKIP-T 712
QY      181 SMHPLYRK-----IIVLSVLAIGICTAYLILPMPVYKNMESQNTKIILGCNEIS 232
Db      713 SFH---RKWGLNLQFLVFLCTFMQIVICVILWYTAPPSSYRNHELEDEIIFITCHEGS 769
QY      233 IEFLYSMFIDAFALLCLFLTTFVARQLPDNYYEGKCTTFGLMVFPIIWMSPVPVYLSTK 292
Db      770 LMAAGSLIGYTCLLAAICFFAFKSRKLPENFNEAKITTFMILFFIVWISFIPAYASTY 829
QY      293 GKFKMAVEIFAILASHGILGCIIPAKCLIIILPERNTSEIVCGRVSTTDCIQLTSAP 352
Db      830 GKFSVAVEVIALAASFGLLACIFENKVIYIILPKSRNTIEEV--RSSTAHAHAKVAARA 887
QY      353 V-----SSELNNTTVS 363
Db      888 TLRRNISRKRSSSLGGSTGS 908

RESULT 2
A56715
calcium receptor (clone pHpCaR-4.0) - human
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 01-Dec-2000
C:Accession: A56715; S49341; A49419; B49419; C49419
R:Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.
J. Biol. Chem. 270, 12919-12925, 1995
A:Title: Molecular cloning and functional expression of human parathyroid calcium receptor
A:Reference number: A56715; MUID:95279439; PMID:7759551
A:Accession: A56715
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1078 <GAR>
R:Pearce, S.H.S.; Thakker, R.V.
submitted to the EMBL Data Library, August 1994
A:Reference number: S49341
A:Accession: S49341
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-180, 'Q', 182-989, 'R', 991-1078 <PEA>
A:CROSS-references: EMBL:X81086
R:Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi,
Cell 75, 1297-1303, 1993
A:Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuric
A:Reference number: A49419; MUID:94094324; PMID:7916660
A:Accession: A49419
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 178-192 <POL>
A:Experimental source: family N
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence modified after extraction from NCBI backbone
A:Note: 186-Arg mutation is associated with familial hypocalciuric hypercalcemia and neo
A:Note: sequence extracted from NCBI backbone (NCBIN:142453)
A:Accession: B49419
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 289-303 <PO2>
A:Experimental source: family E
A:Note: sequence modified after extraction from NCBI backbone
A:Note: 298-Lys mutation is associated with familial hypocalciuric hypercalcemia and neo
A:Note: sequence extracted from NCBI backbone (NCBIN:142455)
A:Accession: C49419
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 788-802 <PO3>
A:Experimental source: family J
A:Note: sequence modified after extraction from NCBI backbone
A:Note: 796-Trp mutation is associated with familial hypocalciuric hypercalcemia and neo
A:Note: sequence extracted from NCBI backbone (NCBIN:142457)
C:Keywords: glycoprotein; receptor; transmembrane protein

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Query Match      35.8%; Score 711.5; DB 2; Length 1078;
Best Local Similarity 38.0%; Pred. No. 8.3e-50;
Matches 145; Conservative 71; Mismatches 139; Indels 27; Gaps 6;

QY      1 LPHSVCTDVCPPGTGRGFVQREBPICCFDSIPCADGHVSRKPGERECEQCQGDYWSNAQKS 60
Db      537 VPFNSCSRCLAGTRKGIIEGETCCFCFCEVCEPDGEYSDTDASACNKPDDPFWSENHNT 596
QY      61 ECVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTAVYVYIHRHTPLVNASDWQGLFIQV 120
Db      597 SCTAKEIEFLSWTEPPFGIALTLFAVLGIFLTAFLGVFKFRNTPIVKATNRELSVLLLF 656
QY      121 SLIIMLLSSMLFIDKPHNWSCHAGQVTLALGFSCLCLSGTKTSSSLFLAYRISKSTQLT 180
Db      657 SLLCCFSSLPFGEPQDWTCLRPAPFGISFVLCISCLVKTNRVLLVF---EAKIP-T 712
QY      181 SMHPLYRK-----IIVLSVLAIGICTAYLILPMPVYKNMESQNTKIILGCNEIS 232
Db      713 SFH---RKWGLNLQFLVFLCTFMQIVICVILWYTAPPSSYRNHELEDEIIFITCHEGS 769
QY      233 IEFLYSMFIDAFALLCLFLTTFVARQLPDNYYEGKCTTFGLMVFPIIWMSPVPVYLSTK 292
Db      770 LMAAGSLIGYTCLLAAICFFAFKSRKLPENFNEAKITTFMILFFIVWISFIPAYASTY 829
QY      293 GKFKMAVEIFAILASHGILGCIIPAKCLIIILPERNTSEIVCGRVSTTDCIQLTSAP 352
Db      830 GKFSVAVEVIALAASFGLLACIFENKVIYIILPKSRNTIEEV--RCSTAHAHAKVAARA 887
QY      353 V-----SSELNNTTVS 364
Db      888 TLRRNISRKRSSSLGGSTGS 909

RESULT 3
B56715
calcium receptor (clone pHpCaR-5.2) - human
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C:Accession: B56715
R:Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.
J. Biol. Chem. 270, 12919-12925, 1995
A:Title: Molecular cloning and functional expression of human parathyroid calcium receptor
A:Reference number: A56715; MUID:95279439; PMID:7759551
A:Accession: B56715
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1088 <GAR>
A:CROSS-references: GB:U20760; NID:9683746; PIDN:AAA86504.1; PID:9683747.
C:Keywords: glycoprotein; receptor; transmembrane protein

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Query Match      35.8%; Score 711.5; DB 2; Length 1088;
Best Local Similarity 38.0%; Pred. No. 8.3e-50;
Matches 145; Conservative 71; Mismatches 139; Indels 27; Gaps 6;

QY      1 LPHSVCTDVCPPGTGRGFVQREBPICCFDSIPCADGHVSRKPGERECEQCQGDYWSNAQKS 60
Db      547 VPFNSCSRCLAGTRKGIIEGETCCFCFCEVCEPDGEYSDTDASACNKPDDPFWSENHNT 606
QY      61 ECVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTAVYVYIHRHTPLVNASDWQGLFIQV 120
Db      607 SCTAKEIEFLSWTEPPFGIALTLFAVLGIFLTAFLGVFKFRNTPIVKATNRELSVLLLF 666
QY      121 SLIIMLLSSMLFIDKPHNWSCHAGQVTLALGFSCLCLSGTKTSSSLFLAYRISKSTQLT 180
Db      667 SLLCCFSSLPFGEPQDWTCLRPAPFGISFVLCISCLVKTNRVLLVF---EAKIP-T 722
QY      181 SMHPLYRK-----IIVLSVLAIGICTAYLILPMPVYKNMESQNTKIILGCNEIS 232
Db      723 SFH---RKWGLNLQFLVFLCTFMQIVICVILWYTAPPSSYRNHELEDEIIFITCHEGS 779
QY      233 IEFLYSMFIDAFALLCLFLTTFVARQLPDNYYEGKCTTFGLMVFPIIWMSPVPVYLSTK 292

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Db 780 LMAFLGLIGVTCLLAAICFFPAPKSKLPENFNEAKFITFSMLIPFIVWISPIPAYASTY 839
QY 293 GKFKMAVEIPAILASSHGLGCIIPAPKCLIIILRPERNTSEIVCGRVSTTDCNCIQLTSAP 352
Db 840 GRFVSAVEVIAILAAISFGLLACIFFNKKYIILFKPSRNTIEEV--RCSTAAHAFKVAARA 897
QY 353 V-----SSELNNTTVST 364
Db 898 TLRRSNVSRKSSSLGGSTGST 910
RESULT 4
S40476
Ca(2+)-sensing receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S40476
R:Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.; H
Nature 366, 575-580, 1993
A:Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor from b
A:Reference number: S40476; MUID:94077182; PMID:8255296
A:Accession: S40476
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1085 <BRO>
A:Cross-references: UNIPROT:P35384; GB:S67307; NID:G453108; PIDN:AAB29171.1; PID:G453109
Query Match 35.7%; Score 709.5; DB 2; Length 1085;
Best Local Similarity 38.0%; Pred. No. 1.2e-49;
Matches 145; Conservative 72; Mismatches 138; Indels 27; Gaps 6;
QY 1 LPHSVCTDVCPPGTGRGFGVQREBPICDFSIIPCADGHVSRKPGRECEQCGEDYWSNAQKS 60
Db 538 VPPNSCRDCLAGTRKGIIEGRTCCFCEVCPDGEYSDETDASACDKCPDDFWSNENHT 597
QY 61 ECVLKEVEIAYDEALGFTLVLSVFGAFVIAVTAAYVYHRTPLVNASDQGLFLIOV 120
Db 598 SCIAKEIBELSWTEPFGIALTLFAVLGIFLTAFLVGLVFIFKFRNTPIVKATNRELSYLLLF 657
QY 121 SLIIMLSMLPFDKPHNWSMAGQVTLALGFLSLCLSGKTSLSFLAYRISKSTQLT 180
Db 658 SLICCFSSSLFFIGEPQDWTCRLRQAPGISFVLCISLIVKTNRVLLVF--EAKIP-T 713
QY 181 SMHPLYRK-----IIVLSVLAIEGICTAYLILEPMPVYKNMESQNTKIILGNETS 232
Db 714 SFH---RKWGLNLQLLVFLCTFMQIVICAIWLTAPSSYRNHELEDEIIFITCHEGS 770
QY 233 IFLYSMFGIDAFIALLCFLTTFVARQLPDNYEGKCTIFGMLVFFIIMSVFVYLSK 292
Db 771 LMAFLGLIGVTCLLAAICFFPAPKSKLPENFNEAKFITFSMLIPFIVWISPIPAYASTY 830
QY 293 GKFKMAVEIPAILASSHGLGCIIPAPKCLIIILRPERNTSEIVCGRVSTTDCNCIQLTSAP 352
Db 831 GRFVSAVEVIAILAAISFGLLACIFFNKKYIILFKPSRNTIEEV--RCSTAAHAFKVAARA 898
QY 353 V-----SSELNNTTVST 364
Db 898 TLRRSNVSRKSSSLGGSTGST 910
RESULT 5
JC7683
taste receptor TIR3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: JC7683
R:Kitagawa, M.; Kusakabe, Y.; Miura, H.; Ninomiya, Y.; Hino, A.
Biochem. Biophys. Res. Commun. 283, 236-242, 2001
A:Title: Molecular genetic identification of a candidate receptor gene for sweet taste.
A:Reference number: JC7683; MUID:21222875; PMID:11322794
A:Contents: tongue
A:Accession: JC7683
A:Molecule type: mRNA

A:Residues: 1-858 <KIT>
A:Cross-references: UNIPROT:Q91VA4; DBJ:AB049994
C:Comment: This protein, a seven-transmembrane receptor, serves as a mediator of the si
C:Genetics:
A:Gene: tlr3
A:Map position: 4
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: transmembrane protein
Query Match 21.7%; Score 431.5; DB 2; Length 858;
Best Local Similarity 30.6%; Pred. No. 3.5e-27;
Matches 105; Conservative 66; Mismatches 163; Indels 9; Gaps 3;
QY 1 LPHSVCTDVCPPGTGR---GFGVQREBPICDFSIIPCADGHVSRKPGRECEQCGEDYWSNA 57
Db 499 VFPVSQCSROCKDQGVRRVKGPHS----CCYDCVCKAGSYRKHDPDFTCTPCNQDQMSPE 554
QY 58 QKSECVLKEVEIAYDEALGFTLVLSVFGAFVIAVTAAYVYHRTPLVNASDQGLFL 117
Db 555 KSTACLPKRPKFLANGEPVLSLMLLLCLVLGALAAALGLSVHHWDSPLVQASGGSQFCF 614
QY 118 IQVSLIIMLSMLPFDKPHNWSMAGQVTLALGFLSLCLSGKTSLSFLAYR--ISK 175
Db 615 GLICGLFCLSVLLPGRPSSASCLAQQPMALPLTGLCLSTLFLQAAETFFVSESLPSWA 674
QY 176 KTQLTSMHPLYRKIIIVLSVLAIEGICTAYLILEPMPVYKNMESQNTKIILGNETSIEF 235
Db 675 NWLSYLRGLMAWLVLLATFVEALCAWYLIAPPEVVDWSVLPTVELEHCHVRSWYS 734
QY 236 LYSMFGIDAFIALLCFLTTFVARQLPDNYEGKCTIFGMLVFFIIMSVFVYLSK 295
Db 735 LCLVHITNMLAFLCFLGTFVQSQGRYNRARGLTFAMLAYFITWVSFVPLLANVQVAY 794
QY 296 KMAVEIPAILASSHGLGCIIPAPKCLIIILRPERNTSEIVCGR 338
Db 795 OPVQMGAILVCALGILVTFHLPRCYVLLWLPKLTQBFLLGR 837
RESULT 6
JC7160
metabotropic glutamate receptor subtype 3 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C:Accession: JC7160
R:Minoshima, T.; Nakanishi, S.
J. Biochem. 126, 889-896, 1999
A:Title: Structural organization of the mouse metabotropic glutamate receptor subtype 3
A:Reference number: JC7160; MUID:20012997; PMID:10544282
A:Accession: JC7160
A:Molecule type: DNA
A:Residues: 1-879 <MIN>
A:Cross-references: GB:AF170696
C:Genetics:
A:Gene: mGluR3
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: differentiation; G protein-coupled receptor; receptor; transmembrane protei
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-879/Product: metabotropic glutamate receptor subtype 3 #status predicted <MAT>
F:577-599/Domain: transmembrane #status predicted <TM1>
F:614-634/Domain: transmembrane #status predicted <TM2>
F:646-664/Domain: transmembrane #status predicted <TM3>
F:689-709/Domain: transmembrane #status predicted <TM4>
F:735-756/Domain: transmembrane #status predicted <TM5>
F:770-791/Domain: transmembrane #status predicted <TM6>
F:804-828/Domain: transmembrane #status predicted <TM7>
Query Match 20.9%; Score 415.5; DB 2; Length 879;
Best Local Similarity 29.1%; Pred. No. 7.2e-26;
Matches 111; Conservative 69; Mismatches 179; Indels 23; Gaps 9;
QY 1 LPHSVCTDVCPPGTGRGFGVQREBPICDFSIIPCADGHVSRKPGRECEQCGEDYWS 55
Db 504 VPTSQSDPCAFNEMKN-MQPGDVCCWICIPC-----EPVEYLVDFTCMDCGPGWP 555

Db 791 TTTMCVSVLSGVSGLVLCIFAPKLHILFQPKN-----VVSHRAPTSRFGSAAPRASANLIG 847

QY 355 SELNNTTVSVLDDRLVI 372

Db 848 QSGSQPVTVCNGREV 865

RESULT 9

JC2132

metabotropic glutamate receptor 5 A - human

C:Species: Homo sapiens (man)

C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996

C:Accession: JC2132

R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.

Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994

A:Title: Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor

A:Reference number: JC2131; MUID:94197696; PMID:7908515

A:Accession: JC2132

A:Molecule type: mRNA

A:Residues: 1-1180 <MIN>

C:Comment: This protein is coupled to guanine nucleotide binding proteins.

C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein

F:580-604/Domain: transmembrane #status predicted <TM1>

F:617-637/Domain: transmembrane #status predicted <TM2>

F:644-664/Domain: transmembrane #status predicted <TM3>

F:694-714/Domain: transmembrane #status predicted <TM4>

F:738-759/Domain: transmembrane #status predicted <TM5>

F:773-794/Domain: transmembrane #status predicted <TM6>

F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 20.0%; Score 397.5; DB 2; Length 1180;

Best Local Similarity 28.9%; Pred. No. 2.8e-24;

Matches 99; Conservative 67; Mismatches 158; Indels 19; Gaps 7;

QY 4 SVCTDVCPPGTGRGVQREPICCFDSIPCADGHVSRKPGRECEQCQGDYWSNAKSECV 63

Db 509 SVCSEPCERKQIKVIRKGEVSCCWTCTCKENEYVQ--DEYTKACQLGSWPTDDLTGCD 566

QY 64 LKEVEYLAVDEALGFTLVLSVFGAFVVLAVTAVVYVHHTPLVNASDWQLGFLIQVSLI 123

Db 567 LIPQVLRGDDPEIAVFAVCLGLLATLFTVTVFIYRDTFVVKSSRELCTVILLAGIC 626

QY 124 IMLSSMLFIDKPHNWSMAGQVTLALGFLSLCLSGKTSLSFLAYRISKSTQJTSMH 183

Db 627 LGVLCFTCLIAKPKQIVCYLQRIIGLSPAMSYSLVTKTNR--IARILAGSKKIKCTKK 684

QY 184 PLY-----RKIIVLISVLAIEIGICTAYLILEPPMVYKNMESQNTKIILGCNEISIFLYS 238

Db 685 PRFMSACQLVIAFILIICQLGHVAFIMEPPDIMEHDYPSIR-EVYLICNTTNLG-VVT 742

QY 239 MFGIDAPLALLCFLTTFVARQLPDNYVEGKCTIFGMLVFPFIWMSVPVYVLTSTGKFKMA 298

Db 743 PLGYNGLLILSCYFYAFKTRNVPANFNKAYIAFTWYTCIIWLAFVPIYFGS--NYKII 800

QY 299 VEIFAILASHGHLGCFAPKCLIIILRPERN-----TSEIV 335

Db 801 TMCFSVLSATVALGCMFVPKVIILAKPERNRSAPFTSTVV 843

RESULT 10

A41939

G protein-coupled glutamate receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A41939; S15362

R:Houamed, K.M.; Kujper, J.L.; Gilbert, T.L.; Haideman, B.A.; O'Hara, P.J.; Mulvihill, Science 252, 1318-1321, 1991

A:Title: Cloning, expression, and gene structure of a G protein-coupled glutamate receptor

A:Reference number: A41939; MUID:92022526; PMID:1656524

A:Accession: A41939

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-1199 <HOU>

A:Cross-references: UNIPROT:P23385; GB:M61099; NID:G397806; PIDN:AAA19497.1; PID:G20446;

A:Experimental source: cerebellum

A>Note: sequence extracted from NCBI backbone (NCBIP:60785)

R:Masu, M.; Tanabe, Y.; Tsuchida, K.; Shigemoto, R.; Nakanishi, S.

Nature 349, 760-765, 1991

A:Title: Sequence and expression of a metabotropic glutamate receptor.

A:Reference number: S15362; MUID:91156047; PMID:1847995

A:Accession: S15362

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1199 <MAS>

A:Cross-references: EMBL:X57569; NID:G56646; PIDN:CAA40799.1; PID:G56647

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 20.0%; Score 397.5; DB 2; Length 1199;

Best Local Similarity 28.6%; Pred. No. 2.9e-24;

Matches 98; Conservative 69; Mismatches 157; Indels 19; Gaps 7;

QY 4 SVCTDVCPPGTGRGVQREPICCFDSIPCADGHVSRKPGRECEQCQGDYWSNAKSECV 63

Db 522 SVCSEPCERKQIKVIRKGEVSCCWTCTCKENEYVQ--DEFTCRACDLGWPNAELTGCE 579

QY 64 LKEVEYLAVDEALGFTLVLSVFGAFVVLAVTAVVYVHHTPLVNASDWQLGFLIQVSLI 123

Db 580 PIPVRYLEWSDIESIAFAFSCGLILVTLFVTLFVLYRDTFVVKSSRELCTVILLAGIF 639

QY 124 IMLSSMLFIDKPHNWSMAGQVTLALGFLSLCLSGKTSLSFLAYRISKSTQJTSMH 183

Db 640 LGVCPFTLIARPTTSCYQLQRLVGLSSAMCYSLVTKTNR--IARILAGSKKIKCTRK 697

QY 184 PLY-----RKIIVLISVLAIEIGICTAYLILEPPMVYKNMESQNTKIILGCNEISIFLYS 238

Db 698 PRFMSAWAVIIASILISVQLTLVTLIIMEPPMILSYPSIK-EVYLICNTSNLG-VVA 755

QY 239 MFGIDAPLALLCFLTTFVARQLPDNYVEGKCTIFGMLVFPFIWMSVPVYVLTSTGKFKMA 298

Db 756 PVGYNGLLIMSTYFYAFKTRNVPANFNKAYIAFTWYTCIIWLAFVPIYFGS--NYKII 813

QY 299 VEIFAILASHGHLGCFAPKCLIIILRPERN-----TSEIV 335

Db 814 TTCFAVLSVTVLALGCMFVPKVIILAKPERNRSAPFTSDVV 856

RESULT 11

JC2131

metabotropic glutamate receptor 5 B - human

C:Species: Homo sapiens (man)

C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996

C:Accession: JC2131

R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.

Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994

A:Title: Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor

A:Reference number: JC2131; MUID:94197696; PMID:7908515

A:Accession: JC2131

A:Molecule type: mRNA

A:Residues: 1-1212 <MIN>

C:Comment: This protein is coupled to guanine nucleotide binding proteins.

C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein

F:580-604/Domain: transmembrane #status predicted <TM1>

F:617-637/Domain: transmembrane #status predicted <TM2>

F:644-664/Domain: transmembrane #status predicted <TM3>

F:694-714/Domain: transmembrane #status predicted <TM4>

F:738-759/Domain: transmembrane #status predicted <TM5>

F:773-794/Domain: transmembrane #status predicted <TM6>

F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 20.0%; Score 397.5; DB 2; Length 1212;

Best Local Similarity 28.9%; Pred. No. 2.9e-24;

Matches 99; Conservative 67; Mismatches 158; Indels 19; Gaps 7;

QY 4 SVCTDVCPPGTGRGVQREPICCFDSIPCADGHVSRKPGRECEQCQGDYWSNAKSECV 63

Db 509 SVCSEPCERKQIKVIRKGEVSCCWTCTCKENEYVQ--DEYTKACQLGSWPTDDLTGCD 566

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Qy 64 LKEVEYLAYDEALGFTLIVLSVGFVVLAVTAVYVYIHRHTPLVNASDWLGFLIQVSLI 123
Db 567 LIPQYLRWDGPEPIAAVFAFLGLLATLFTVVVFIYRDTPVVKSSRELVIILAGIC 626
Qy 124 IMLSSMLFDIKPHNWSMAGQVTLAIGFSLCLSLGKTSLSFLAVRISKSTQLTSMH 183
Db 627 LGVLTCTCLAKPKQIYCYLQRIIGIGSPAMSYSALVTKTNR--IARILAGSKKICCTKK 684
Qy 184 PLY-----RKIIIVLISLAEIGTAVLIILEPPVYKNMESQNTKIIILGNEISIEFLYS 238
Db 685 PRFWSACQLVIAFILICQLGIIVAFINEPDIDMHDYFSIR-EVLIICNTNLG-VWT 742
Qy 239 MFGIDFLALLCLFLLTFVARQLPDNYEGKCIITFGMLVFFIIIMSVFVYVSLTKGFKQMA 298
Db 743 PLGYNGILLISCTFYAKTRKRVNPFANFNAKYIAFTWVTTCTIILWLAFFVIYFGS--NVKII 800
Qy 299 VEIIFAILASSHGILGCIIFAPKCLIIILRPERN-----TSEIV 335
Db 801 TMCFSVLSLSTVALGCMFVKYIIILAKPERNVRSFTTSTVV 843

RESULT 12
A42916
metabotropic glutamate receptor mGluR5 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A42916
R/Abel, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A/Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5 co
A/Reference number: A42916; MUID:92317054; PMID:1320017
A/Accession: A42916
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1171 <ABE>
A/Cross-references: UNIPROT:P31424; GB:D10891; NID:G220813; PIDN:BAA01711.1; PID:d100218
A/Experimental source: brain
A/Note: sequence extracted from NCBI backbone, NCBIP:107750
C/Keywords: G protein-coupled receptor; transmembrane protein

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C/Species: *Oncorhynchus masou* (cherry salmon)
 C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
 C/Accession: S71376
 C/Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.
 FEBS Lett. 392, 71-76, 1996
 A/Title: Cloning and characterization of a bifunctional metabotropic receptor
 A/Reference number: S71376; MUID:96354880; PMID:8769318

Query Match	19.3%	Score	383;	DB	2;	Length	1218;
Best Local Similarity	27.3%;	Pred.	No. 4.4e-23;				
Matches	98;	Conservative	74;	Mismatches	163;	Indels	24;
Gaps	8						
QY	4	SVCTDVCPPCTGGFVGOREPICDFSDIPCADGHVSRRKPGRERCQCCEGYWSNAQKSRCV	63				
Db	532	SVCSGPCSGKEIKVIIRKGVSCCWICTACKDNELVQ--DEFTTACDLGWWPDPDELEGCE	589				
QY	64	LKEVEYLAVDEALGLFTVLILSVFGAFVVLAVTAIVYIHRHTPLVNASDWQLGFLLIQVSLI	123				
Db	590	PITRLYLEMGNPESIIQQVVFACLIGLVTSPVTIFVLRYRDTPVVKSSRELICYILLAGIF	649				
QY	124	IMLLSSMLFDIKPHNWSCHAGQVTLAIGFSCLISCLLGKTSSLPLAYRIKSKTKOLTSMH	183				
Db	650	LGVICPFPTLIAQPTVASCYLRQLLVLSATMCSALYVTKTNR--IARILAGSKKKICTRK	707				
QY	184	PLY-----RKIIIVLISVLAEGICTAYLILLEPMPVKNMESQNTKIILGCNEISIEFLYS	238				
Db	708	PRFWMAQULVIAGLIVUSVOLTEUVTIILLEPMPVKSYPSIR-EVPLICNTSTVG-NVA	765				
QY	239	MFGIDAFALLCPLTTTFVARQLPDNYEYGKCIITFGMLVFPIIWMSPFPVLTSTRKPKQWA	298				
Db	766	PLGYNGLLIMSCYYIAFKTRNVPAFNFAKYIAFTMYTTCIIWLAFVIPYFGS--NYKII	823				
QY	299	VEIFAILASHGLLCGIPAPKCLIIILRPBN-----TSEIV-----CGRVSTTDNCI	346				
Db	824	TTSFVSLSVTYVALGWCFSPKYYIIILAKEPNNVRSYAFTSDVVVRMHVGDGNVACRSNSL	882				

RESULT 14
T27628

hypothetical protein ZC506.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1993 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T27628
R/Harris, B.
submitted to the EMBL Data Library, December 1994
A/Reference number: Z20395
A/Accession: T27628
A/Status: preliminary; translated from GB/EMBL/DBSJ
A/Molecule type: DNA
A/Residues: 1-999 <WIL>
A/Cross-references: UNIPROT:Q09630; EMBL:Z47073; PIDN:CAA87374.1; GSPDB:GN01
A/Experimental source: clone GSC506

RESULT 13
S71376
glutamate receptor homolog - cherry salmon

C:Superfamily: metabotropic glutamate receptor 4

Query Match 17.8%; Score 353; DB 2; Length 999;
Best Local Similarity 26.3%; Pred. No. 9.8e-21;
Matches 98; Conservative 75; Mismatches 179; Indels 20; Gaps 11;

QY 2 PHSVCTDVCPPGTGRGFVQREPTCCFDSIPCAHGHSVRKPGRECECCGCDYWSNAQKSE 61
DB 607 PVSVCSLPCKKIGFRKQLIKDEQ--CCWACKCED--YEYLINETHCVGCEQGWMPPTKDRKG 663

QY 62 CV---LKEVEYLAVDEALGFTLLVLSVEGAFVVLAVTAVVVIHRRHTPLVNASDWLQGLFI 118
DB 664 CFDLSLSQLKMRWSMYSVPTILAVFGIIATLFVIVVVIYNEIPVVKASGRELSIYL 723

QY 119 QVSLIIMLSSMLPIDKPHNWSMCAGQVTLALGFSCLCLGKTSLSFLAYRISKRTQ 178
DB 724 LISIMCYCMTFVLLSKPSAIVCAIKRTGIGPAFSCLYSAMFVKTNRIFRIS--TRSAQR 782

QY 179 LTSWHPYLRKIIIVLISVLAIGICTA--YLLEPPMVYKMWESQNTKIILGCNEISIEFL 236
DB 783 PRFISPISQ--VVMTAMLAGVQLIGLSLWLSVVP--GWRHHYPTRDQVVLTCNVPDHHFL 839

QY 237 YSMFGIDAFLLALCFLLTTFVARQLPONYEGKCTITGMLVFFIIMWSFVPLYLSTKGKPK 296
DB 840 YSL-AYDGFLLIVCTYVAVKTRKVPENFETKEIGFSMTTTCVWLWSLWIFFFGTQSDFO 898

QY 297 MAYE--IFAILASHGLGICIPAKCLIIILLRPERNT---SEIVGRYS--TTDNCIQT 349
DB 899 IQTSSLCISMSANVALCIFSPKLIWILFEKHKNVRKQEGGSMLNKSSRLGNCSSRL 958

QY 350 SAFVSSSELNNTT 361
DB 959 CANSIDEPNOYT 970

RESULT 15
A49874
metabotropic glutamate receptor 7 - rat
N;Alternate names: metabotropic glutamate receptor mGluR7
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: A49874; I57954
R;Okamoto, N.; Hori, S.; Akazawa, C.; Hayaashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, J. Biol. Chem. 269, 1231-1236, 1994
A;Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 coupled to phospholipase C- β 1
A;Reference number: A49874; MUID:94117433; PMID:8288585
A;Accession: A49874
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-915 <RES>
A;Cross-references: UNIPROT:P35400; GB:D16817; NID:G458728; PIDN:BAA04092.1; PID:G458729
R;Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L. Mol. Pharmacol. 45, 367-372, 1994
A;Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid receptor family
A;Reference number: I57954; MUID:94195260; PMID:8145723
A;Accession: I57954
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-915 <RES>
A;Cross-references: EMBL:U06832; NID:G459657; PIDN:AAA20655.1; PID:G459658
C;Genetics:
A;Gene: MGLUR7
C;Superfamily: metabotropic glutamate receptor 4
C;Keywords: neurotransmitter receptor

Query Match 16.3%; Score 324; DB 2; Length 915;
Best Local Similarity 26.1%; Pred. No. 2e-18;
Matches 93; Conservative 71; Mismatches 153; Indels 40; Gaps 12;

QY 1 LPHSVCTDVCPPGTGRGFVQREPTCCFDSIPCAHGHSVRKPGRECECCGCDYWSNAQKS 60
DB 518 IPSVSVCTLPCKPGQ--RKTKTGKTPCCWTCBPC--DGY-QYQFDQMTQCHQCPYDORPNEVT 574

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